BAYESIAN GENETIC MAPPING

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Many aspects in plant and animal breeding such as QTL detection rely on the availability of reliable and accurate genetic maps. The ordering of molecular markers in a map is based on the calculation of the proportion of offspring different to their parents. This parameter is called "recombination fraction". The process of obtaining a genetic map implies estimating the recombination fractions (distances) between all pairs of markers and, based on these estimates, placing the markers in a linear map. We have developed a Bayesian model to estimate recombination fractions among all markers within a linkage group and also an algorithm to obtain the genetic map in a multipoint manner. We consider here Backcross and F_2 crosses with both codominant and dominant markers. Simulated data of different sample sizes (50, 100 and 200 individuals) has been used to test the methodology. Sampling distributions of the posterior mean and order show good agreement between observed and expected values even with the smallest sample size.